1600

P.6

#12

RAW SEQUENCE LISTING
DATE: 04/17/2003
PATENT APPLICATION: **US/09/284,327A**
TIME: 10:41:38

Input Set : **A:\GC516-2-US-SEQLIST.txt**
Output Set: **N:\CRF4\04172003\I284327A.raw**

```
 4 <110> APPLICANT: Bower, Benjamin S.
 5         Fowler, Timothy
 6         Phillips, Jay I.
 8 <120> TITLE OF INVENTION: Novel EGIII-Like Enzymes, DNA Encoding
 9         Such Enzymes and Methods for Producing Such Enzymes
12 <130> FILE REFERENCE: GC516-2-US
14 <140> CURRENT APPLICATION NUMBER: US 09/284,327A
15 <141> CURRENT FILING DATE: 1999-04-10
17 <150> PRIOR APPLICATION NUMBER: PCT/US98/26552
18 <151> PRIOR FILING DATE: 1998-12-14
20 <160> NUMBER OF SEQ ID NOS: 68
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 5
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: synthetic
```
W--> `32 <221> NAME/KEY: VARIANT`
```
33 <222> LOCATION: 3
34 <223> OTHER INFORMATION: Xaa = Leu, Phe, Lys, or Ile
```
W--> `36 <400> 1`
W--> `37 Asn Asn Xaa Trp Gly`
```
38  1            5
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 5
42 <212> TYPE: PRT
43 <213> ORGANISM: Artificial Sequence
45 <220> FEATURE:
46 <223> OTHER INFORMATION: synthetic
```
W--> `48 <221> NAME/KEY: VARIANT`
```
49 <222> LOCATION: 2
50 <223> OTHER INFORMATION: Xaa = Leu, Phe, or Ile
```
W--> `52 <400> 2`
W--> `53 Glu Xaa Met Ile Trp`
```
54  1            5
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 6
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: synthetic
64 <400> SEQUENCE: 3
```

```
65 Gly Thr Glu Pro Phe Thr
66  1                    5
68 <210> SEQ ID NO: 4
69 <211> LENGTH: 5
70 <212> TYPE: PRT
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: synthetic
76 <400> SEQUENCE: 4
77 Ser Val Lys Ser Tyr
78  1                    5
80 <210> SEQ ID NO: 5
81 <211> LENGTH: 6
82 <212> TYPE: PRT
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: synthetic
88 <400> SEQUENCE: 5
89 Lys Asn Phe Phe Asn Tyr
90  1                    5
92 <210> SEQ ID NO: 6
93 <211> LENGTH: 702
94 <212> TYPE: DNA
95 <213> ORGANISM: Trichoderma reesei
97 <400> SEQUENCE: 6
 98 atgaagttcc ttcaagtcct ccctgccctc ataccggccg ccctggccca aaccagctgt      60
 99 gaccagtggg caaccttcac tggcaacggc tacacagtca gcaacaacct ttggggagca     120
100 tcagccggct ctggatttgg ctgcgtgacg gcggtatcgc tcagcggcgg ggcctcctgg     180
101 cacgcagact ggcagtggtc cggcggccag aacaacgtca agtcgtacca gaactctcag     240
102 attgccattc cccagaagag gaccgtcaac agcatcagca gcatgcccac cactgccagc     300
103 tggagctaca gcgggagcaa catccgcgct aatgttgcgt atgacttgtt caccgcagcc     360
104 aacccgaatc atgtcacgta ctcgggagac tacgaactca tgatctggct tggcaaatac     420
105 ggcgatattg ggccgattgg gtcctcacag ggaacagtca acgtcggtgg ccagagctgg     480
106 acgctctact atggctacaa cggagccatg caagtctatt cctttgtggc ccagaccaac     540
107 actaccaact acagcggaga tgtcaagaac ttcttcaatt atctccgaga caataaagga     600
108 tacaacgctg caggccaata tgttcttagc taccaatttg gtaccgagcc cttcacgggc     660
109 agtggaactc tgaacgtcgc atcctggacc gcatctatca ac                        702
111 <210> SEQ ID NO: 7
112 <211> LENGTH: 232
113 <212> TYPE: PRT
114 <213> ORGANISM: Trichoderma reesei
116 <400> SEQUENCE: 7
117 Met Lys Phe Leu Gln Val Leu Pro Ala Leu Ile Pro Ala Ala Leu Ala
118  1               5                  10                  15
119 Gln Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
120             20                  25                  30
121 Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
122             35                  40                  45
123 Val Thr Ala Val Ser Leu Ser Gly Gly Ala His Ala Asp Trp Gln Trp
```

RAW SEQUENCE LISTING   DATE: 04/17/2003
PATENT APPLICATION: US/09/284,327A   TIME: 10:41:38

Input Set : A:\GC516-2-US-SEQLIST.txt
Output Set: N:\CRF4\04172003\I284327A.raw

```
124       50                    55                    60
125 Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln Ile Ala
126 65                    70                    75                    80
127 Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro Thr Thr
128             85                    90                    95
129 Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val Ala Tyr
130             100                   105                   110
131 Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser Gly Asp
132         115                   120                   125
133 Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly Pro Ile
134     130                   135                   140
135 Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp Thr Leu
136 145                   150                   155                   160
137 Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val Ala Gln
138             165                   170                   175
139 Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe Asn Tyr
140             180                   185                   190
141 Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val Leu Ser
142         195                   200                   205
143 Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu Asn Val
144     210                   215                   220
145 Ala Ser Trp Thr Ala Ser Ile Asn
146 225                   230
148 <210> SEQ ID NO: 8
149 <211> LENGTH: 234
150 <212> TYPE: PRT
151 <213> ORGANISM: Trichoderma reesei
153 <400> SEQUENCE: 8
154 Met Lys Phe Leu Gln Val Leu Pro Ala Leu Ile Pro Ala Ala Leu Ala
155   1                  5                    10                    15
156 Gln Thr Ser Cys Asp Gln Trp Ala Thr Phe Thr Gly Asn Gly Tyr Thr
157             20                    25                    30
158 Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
159             35                    40                    45
160 Val Thr Ala Val Ser Leu Ser Gly Gly Ala Ser Trp His Ala Asp Trp
161     50                    55                    60
162 Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Ser Gln
163 65                    70                    75                    80
164 Ile Ala Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Ser Ser Met Pro
165             85                    90                    95
166 Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asn Ile Arg Ala Asn Val
167             100                   105                   110
168 Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
169         115                   120                   125
170 Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
171     130                   135                   140
172 Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Ser Trp
173 145                   150                   155                   160
174 Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
```

RAW SEQUENCE LISTING   DATE: 04/17/2003
PATENT APPLICATION: US/09/284,327A   TIME: 10:41:38

Input Set : A:\GC516-2-US-SEQLIST.txt
Output Set: N:\CRF4\04172003\I284327A.raw

```
175                 165                 170                 175
176 Ala Gln Thr Asn Thr Thr Asn Tyr Ser Gly Asp Val Lys Asn Phe Phe
177         180                 185                 190
178 Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Ala Gly Gln Tyr Val
179         195                 200                 205
180 Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
181     210                 215                 220
182 Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
183 225                 230
185 <210> SEQ ID NO: 9
186 <211> LENGTH: 234
187 <212> TYPE: PRT
188 <213> ORGANISM: Hypocrea schweinitzii
190 <400> SEQUENCE: 9
191 Met Lys Phe Leu Gln Val Leu Pro Ala Ile Leu Pro Ala Ala Leu Ala
192 1               5                   10                  15
193 Gln Thr Ser Cys Asp Gln Tyr Ala Thr Phe Ser Gly Asn Gly Tyr Ile
194         20                  25                  30
195 Val Ser Asn Asn Leu Trp Gly Ala Ser Ala Gly Ser Gly Phe Gly Cys
196         35                  40                  45
197 Val Thr Ser Val Ser Leu Asn Gly Ala Ala Ser Trp His Ala Asp Trp
198     50                  55                  60
199 Gln Trp Ser Gly Gly Gln Asn Asn Val Lys Ser Tyr Gln Asn Val Gln
200 65                  70                  75                  80
201 Ile Asn Ile Pro Gln Lys Arg Thr Val Asn Ser Ile Gly Ser Met Pro
202                 85                  90                  95
203 Thr Thr Ala Ser Trp Ser Tyr Ser Gly Ser Asp Ile Arg Ala Asn Val
204             100                 105                 110
205 Ala Tyr Asp Leu Phe Thr Ala Ala Asn Pro Asn His Val Thr Tyr Ser
206         115                 120                 125
207 Gly Asp Tyr Glu Leu Met Ile Trp Leu Gly Lys Tyr Gly Asp Ile Gly
208     130                 135                 140
209 Pro Ile Gly Ser Ser Gln Gly Thr Val Asn Val Gly Gly Gln Thr Trp
210 145                 150                 155                 160
211 Thr Leu Tyr Tyr Gly Tyr Asn Gly Ala Met Gln Val Tyr Ser Phe Val
212             165                 170                 175
213 Ala Gln Ser Asn Thr Thr Ser Tyr Ser Gly Asp Val Lys Asn Phe Phe
214         180                 185                 190
215 Asn Tyr Leu Arg Asp Asn Lys Gly Tyr Asn Ala Gly Gly Gln Tyr Val
216         195                 200                 205
217 Leu Ser Tyr Gln Phe Gly Thr Glu Pro Phe Thr Gly Ser Gly Thr Leu
218     210                 215                 220
219 Asn Val Ala Ser Trp Thr Ala Ser Ile Asn
220 225                 230
222 <210> SEQ ID NO: 10
223 <211> LENGTH: 259
224 <212> TYPE: PRT
225 <213> ORGANISM: Aspergillus aculeatus
227 <400> SEQUENCE: 10
```

```
228 Met Lys Ala Phe His Leu Leu Ala Ala Leu Ala Gly Ala Ala Val Ala
229 1               5                   10              15
230 Gln Gln Ala Gln Leu Cys Asp Gln Tyr Ala Thr Tyr Thr Gly Gly Val
231             20                  25              30
232 Tyr Thr Ile Asn Asn Asn Leu Trp Gly Lys Asp Ala Gly Ser Gly Ser
233             35                  40              45
234 Gln Cys Thr Thr Val Asn Ser Ala Ser Ser Ala Gly Thr Ser Trp Ser
235     50                  55                  60
236 Thr Lys Trp Asn Trp Ser Gly Gly Glu Asn Ser Val Lys Ser Tyr Ala
237 65                  70                  75                  80
238 Asn Ser Gly Leu Thr Phe Asn Lys Lys Leu Val Ser Gln Ile Ser Gln
239             85                  90                  95
240 Ile Pro Thr Thr Ala Arg Trp Ser Tyr Asp Asn Thr Gly Ile Arg Ala
241             100                 105                 110
242 Asp Val Ala Tyr Asp Leu Phe Thr Ala Ala Asp Ile Asn His Val Thr
243             115                 120                 125
244 Trp Ser Gly Asp Tyr Glu Leu Met Ile Trp Leu Ala Arg Tyr Gly Gly
245     130                 135                 140
246 Val Gln Pro Ile Gly Ser Gln Ile Ala Thr Ala Thr Val Asp Gly Gln
247 145                 150                 155                 160
248 Thr Trp Glu Leu Trp Tyr Gly Ala Asn Gly Ser Gln Lys Thr Tyr Ser
249             165                 170                 175
250 Phe Val Ala Pro Thr Pro Ile Thr Ser Phe Gln Gly Asp Val Asn Asp
251             180                 185                 190
252 Phe Phe Lys Tyr Leu Thr Gln Asn His Gly Phe Pro Ala Ser Ser Gln
253             195                 200                 205
254 Tyr Leu Ile Thr Leu Gln Phe Gly Thr Glu Pro Phe Thr Gly Gly Pro
255     210                 215                 220
256 Ala Thr Leu Ser Val Ser Asn Trp Ser Ala Ser Val Gln Gln Ala Gly
257 225                 230                 235                 240
258 Phe Glu Pro Trp Gln Asn Gly Ala Gly Leu Ala Val Asn Ser Phe Ser
259             245                 250                 255
260 Ser Thr Val
263 <210> SEQ ID NO: 11
264 <211> LENGTH: 239
265 <212> TYPE: PRT
266 <213> ORGANISM: Aspergillus kawachii (1)
268 <400> SEQUENCE: 11
269 Met Lys Leu Ser Met Thr Leu Ser Leu Phe Ala Ala Thr Ala Met Gly
270 1               5                   10              15
271 Gln Thr Met Cys Ser Gln Tyr Asp Ser Ala Ser Ser Pro Pro Tyr Ser
272             20                  25              30
273 Val Asn Gln Asn Leu Trp Gly Glu Tyr Gln Gly Thr Gly Ser Gln Cys
274             35                  40                  45
275 Val Tyr Val Asp Lys Leu Ser Ser Ser Gly Ala Ser Trp His Thr Lys
276     50                  55                  60
277 Trp Thr Trp Ser Gly Gly Glu Gly Thr Val Lys Ser Tyr Ser Asn Ser
278 65                  70                  75                  80
279 Gly Leu Thr Phe Asp Lys Lys Leu Val Ser Asp Val Ser Ser Ile Pro
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/17/2003
PATENT APPLICATION: **US/09/284,327A**   TIME: 10:41:39

Input Set : **A:\GC516-2-US-SEQLIST.txt**
Output Set: **N:\CRF4\04172003\I284327A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:1; Xaa Pos. 3
Seq#:2; Xaa Pos. 2
Seq#:30; N Pos. 9
Seq#:31; N Pos. 9
Seq#:32; N Pos. 12
Seq#:33; N Pos. 6
Seq#:34; N Pos. 10
Seq#:35; N Pos. 9
Seq#:36; N Pos. 10
Seq#:37; N Pos. 6
Seq#:38; N Pos. 6
Seq#:39; N Pos. 6
Seq#:40; N Pos. 6
Seq#:41; N Pos. 12,15
Seq#:42; Xaa Pos. 1,2,3,4,5
Seq#:60; Xaa Pos. 6
Seq#:64; Xaa Pos. 1
Seq#:65; Xaa Pos. 4
Seq#:68; Xaa Pos. 4
```
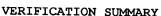
VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/284,327A**

DATE: 04/17/2003
TIME: 10:41:39

Input Set : **A:\GC516-2-US-SEQLIST.txt**
Output Set: **N:\CRF4\04172003\I284327A.raw**

```
L:32 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:48 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:52 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:1046 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1050 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1061 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1065 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:1066 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1076 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1080 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32
L:1081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1091 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1095 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:1096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1106 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1110 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1121 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1125 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1136 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1140 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:1141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1151 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1155 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37
L:1156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1166 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:38
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:1181 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1185 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:39
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:1196 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1200 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:40
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0
L:1211 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1215 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41
L:1216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:1226 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1230 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:1234 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:1238 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:1242 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:1246 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/284,327A**

DATE: 04/17/2003
TIME: 10:41:39

Input Set : **A:\GC516-2-US-SEQLIST.txt**
Output Set: **N:\CRF4\04172003\I284327A.raw**

```
L:1247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:1623 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1627 M:258 W: Mandatory.Feature missing, <220> Tag not found for SEQ ID#:60
L:1628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:0
L:1707 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1711 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:64
L:1712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0
L:1723 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1727 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:65
L:1728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0
L:1763 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1767 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:68
L:1768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0
```